ENHANCED EXPRESSION

TECHNICAL FIELD

The present invention relates generally to methods and materials for boosting gene expression.

BACKGROUND ART

In plants, post-transcriptional gene silencing (PTGS) is manifested as the reduction in steady-state levels of specific RNAs after introduction of homologous sequences in the plant genome. This reduction is caused by an increased turnover of target RNA species, with the transcription level of the corresponding genes remaining unaffected.

It is known that suppressing PTGS e.g. by mutating or otherwise impairing the function of the mechanistic genes which support it will increase the expression of silenced genes, back to non-silenced levels.

For example the SGS2 and SGS3 genes were found by mutation of a silenced *A. thaliana* plant line containing nptII/p35S/uidA/tRBC (Elmayan, *et al.* 1998). GUS activity was restored after mutation. The SDE1 and SDE3 genes were found by mutation of a silenced plant line containing p35S/PVX:GFP amplicon and p35S/GFP (Dalmay, *et al.* 2000b). GFP fluorescence was restored after mutation.

Nevertheless, it will be appreciated that methods of increasing the expression of genes over and above those achieved even in such silencing defective contexts would provide a contribution to the art.

DISCLOSURE OF THE INVENTION

The present inventors have discovered that expression of a target gene in a PTGS-suppressed background can be additionally enhanced by the use of Matrix Attachment Regions (MARs). MARs are non-transcribed regions in eukaryotic genomes that are attached to the proteinaceous matrix in the nucleus (reviewed by Holmes-Davis & Comai, 1998; Allen *et al.*, 2000).

It has been hypothesized in the art that MARs may have a role in shielding sequences from gene silencing. In some cases, transgene expression dropped when MARs were removed from homozygous, high-expressing transgenic tobacco lines (Mlynarova *et al.*, 2003 The Plant Cell: 15, 2203-2217). However, when MARs were used to flank vector constructs for transformation of *Arabidopsis thaliana*, no PTGS-shielding effect was observed in populations of hemizygous, primary transformants (De Bolle & Butaye *et al.* (2003)).

Irrespective of the results above, it was not known or expected that MARs could further enhance expression in contexts in which silencing was impaired by a different mechanism.

Briefly, the present inventors demonstrated that the influence of MARs on the level and the variability of gene expression in *Arabidopsis thaliana* differed significantly between wild-type plants and various *A. thaliana* mutants impaired in the RNA silencing mechanism, with much greater levels of expression being shown by the latter. In one embodiment of the invention it was estimated that GUS expression was enhanced to the extent that the protein accumulated to roughly 10% of the total soluble proteins in the vegetative tissues of transgenic plants.

Particular aspects of, and definitions used in, the invention will now be discussed in more detail.

In general the invention provides a method of producing a transgenic organism in which a target nucleotide sequence is expressed at an enhanced level, the method comprising the steps of:
(i) providing an organism in which PTGS has been suppressed (which suppression may be pre-existing, or may require the step of suppressing PTGS in the organism e.g. using the methods discussed below),
(ii) associating said target nucleotide sequence with one or more heterologous Matrix Attachment Region (MARs), and optionally:
(iii) causing or permitting expression from the target nucleotide sequence in the organism.

Thus, for example, the invention provides a method of achieving enhanced expression of a heterologous target nucleotide sequence in an organism which is deficient in one or more genes required to support PTGS, which method comprises the steps of associating said target nucleotide sequence with one or more MARs. In one embodiment, the or each of the MARs may be introduced to and associated at random with a pre-existing gene present in the genome of the organism (e.g. to positions flanking it).

The target nucleotide sequence may be one which is endogenous, but is operably linked to a strong, heterologous promoter or enhancer sequence. Such methods may involve:
(i) providing an organism in which PTGS has been, or is suppressed (as discussed herein),
(iia) operably linking said target nucleotide sequence with a heterologous strong promoter or enhancer sequence, and
(iib) associating said target nucleotide sequence with one or more MARs.

Such methods could be performed analogously to existing studies where e.g. the 35S- promoter is introduced at random into a genome to alter

the expression of neighbouring endogenous genes, "endogenes"; or e.g. activation-tagging in which enhancers of the p35S are randomly inserted into a genome to activate/increase the expression of endogenes for selection of altered phenotypes (Weigel, D., *et al.* (2000) Activation tagging in Arabidopsis. Plant Physiol., 122: 1003-13.).

In one embodiment this may be carried out as follows:
(i) providing an organism in which PTGS has been, or is suppressed (as discussed herein),
(iia) providing a target nucleic acid construct comprising (a) a promoter, and (b) one or more Matrix Attachment Regions (MARs) associated therewith,
(iib) introducing said target construct into a cell of the organism, such that the promoter becomes operably linked to an endogenous target nucleotide sequence.

In another, preferred embodiment, the target nucleotide sequence and promoter will both be heterologous to the organism. Thus this aspect of the invention provides a method of producing a transgenic organism in which a heterologous target nucleotide sequence is expressed at an enhanced level, the method comprising the steps of:
(i) providing an organism in which PTGS has been suppressed,
(iia) providing a target nucleic acid construct comprising (a) an expression cassette including the target nucleotide sequence operably linked to a promoter, and (b) one or more Matrix Attachment Regions (MARs) associated therewith,
(iib) introducing said target construct into a cell of the organism.

In principle the steps of the method may be carried out in any order i.e. the PTGS may be suppressed after introduction of the construct. Thus the invention provides the steps of:
(i) providing an organism,

(iia) associating the target nucleotide sequence with one or more MARs in a cell of the organism as discussed above,
(iib) suppressing PTGS in the organism e.g. using the methods discussed below (gene mutation or so on).

However preferably the organism will be one in which PTGS is already suppressed.

In preferred embodiments, the invention is used to enhance expression, particularly the level of translation, of a nucleic acid in a cell, particularly a plant cell. Expression may be enhanced, for instance, by at least about 25-50%, preferably about 50-100%, or more. In certain preferred embodiments at least 5, 10, 15, 20, 25, or 30-fold enhancements of expression may be achieved.

Some particular preferred embodiments will now be discussed.

PTGS suppression

Preferably the organism is one which is deficient in one or more genes required to support PTGS e.g. a plant deficient in one or more of the following:

1) SGS2/SDE1: RdRp (Dalmay *et al.*, 2000, Mourrain *et al.*, 2000)
2) SGS3: coiled coil protein with unknown function (Mourrain *et al.*, 2000)
3) SDE3: RNA helicase (Dalmay *et al.*, 2001)
4) AGO1: PAZ-domain protein (Fagard *et al.*, 2000)
5) WEX: RNAse D (Glazov *et al.*, 2003)

By "deficient" is meant that the activity of the gene (or encoded protein) is impaired. Preferably the gene may be mutated (e.g. a lesion introduced) or otherwise deleted or knocked out. It will be

appreciated that such PTGS suppressed organisms may not be entirely PTGS-deficient. The degree of PTGS impairment or deficiency may be assessed using conventional methods e.g. by monitoring the short RNA species (around 25 nt e.g. about 21-23nt RNA) associated with PTGS, or by monitoring mRNA and\or expressed protein (Northern or Western Blots or a reporter gene such as GFP) the existence and severity of PTGS can be assessed (see Hamilton and Baulcombe 1999).

Other means of generally suppressing or silencing PTGS supporting genes will be known to those skilled in the art, and include the use of viral suppressors of GS such as HC-Pro (Anandalakshmi *et al.*, 1998) and RNAi, which is widely used as a technique to suppress certain target genes and to create 'knock-outs' e.g. in functional genomic programs.

As is well known to those skilled in the art, RNAi can be initiated using hairpin constructs that are designed to trigger PTGS of the target gene, based on homology of sequences (Helliwell and Waterhouse 2003). This technique could therefore also be used to silence genes that play a role in PTGS (e.g. SGS2) in plant lines in which the invention is to be applied. RNAi may be achieved by use of an appropriate vector e.g. a vector comprising part of a nucleic acid sequence encoding a PTGS mechanistic gene, which is suitable for triggering RNAi in the cell. For example the vector may comprise a nucleic acid sequence in both the sense and antisense orientation, such that when expressed as RNA the sense and antisense sections will associate to form a double stranded RNA. This may for example be a long double stranded RNA (e.g., more than 23nts) which may be processed in the cell to produce siRNAs (see for example Myers (2003) *Nature Biotechnology 21:324-328*).

MARs

Optionally only 1 MAR may be associated with the expression cassette, in which case preferably it will be 5′ of the cassette (see e.g. Scöffl e.a. 1993, Transgenic Res. 2, 93-100; van der Geest e.a. 1994, Plant J. 6, 413-423).

Preferably however 2 MARs will be used, which may be the same or different, and which may be from the same or different sources, and these will flank the expression cassette or target nucleotide sequence.

In preferred embodiments the or each MARs will be less than 500, preferably less than 200, and optionally less than 150, 100, or 50 nucleotides upstream of the promoter or downstream of the terminator.

The present invention relates to the use of any MAR origin (e.g. animal, plant, yeast) although preferred examples include that from the the chicken lysozyme gene, or from plants such as petunia and tobacco. Other MARs are reviewed in Holmes-Davis and Comai (1998) and Allen, *et. al* (2000).

Organism

The invention may be applied to any organism in which PTGS can be suppressed, particularly eukaryotic organisms including yeasts, fungi, algae, higher plants. Transformed organisms of the present invention will be non-human. Preferably the organism is a higher plant e.g. Arabidopsis thaliana.

Promoter

Preferably the promoter used to drive the gene of interest will be a strong promoter. Examples of strong promoters for use in plants include:

(1) p35S: Odell *et al.*, 1985

(2) Cassava Vein Mosaic Virus promoter, pCAS, Verdaguer *et al.*, 1996

(3) Promoter of the small subunit of ribulose biphosphate carboxylase, pRbcS: Outchkourov *et al.*, 2003.

However other strong promoters include pUbi (for moncots and dicots) and pActin.

Choice of target genes to enhance

As discussed above, the target gene may be a transgene or an endogene.

Genes of interest include those encoding agronomic traits, insect resistance, disease resistance, herbicide resistance, sterility , grain characteristics, and the like. The genes may be involved in metabolism of oil, starch, carbohydrates, nutrients, etc. Thus genes or traits of interest include, but are not limited to, environmental- or stress- related traits, disease-related traits, and traits affecting agronomic performance. Target sequences also include genes responsible for the synthesis of proteins, peptides, fatty acids, lipids, waxes, oils, starches, sugars, carbohydrates, flavors, odors, toxins, carotenoids, hormones, polymers, flavonoids, storage proteins, phenolic acids, alkaloids, lignins, tannins, celluloses, glycoproteins, glycolipids, etc.

Most preferably the targeted genes in monocots and/or dicots may include those encoding enzymes responsible for oil production in plants such as rape, sunflower, soya bean and maize; enzymes involved in starch synthesis in plants such as potato, maize, cereals; enzymes which synthesise, or proteins which are themselves, natural medicaments such as pharmaceuticals or veterinary products.

Heterologous nucleic acids may encode, *inter alia*, genes of bacterial, fungal, plant or animal origin. The polypeptides may be utilised *in planta* (to modify the characteristics of the plant e.g. with respect to pest susceptibility, vigour, tissue differentiation, fertility, nutritional value etc.) or the plant may be an intermediate for producing the polypeptides which can be purified therefrom for use elsewhere. Such proteins include, but are not limited to retinoblastoma protein, p53, angiostatin, and leptin. Likewise, the methods of the invention can be used to produce mammalian regulatory proteins. Other sequences of interest include proteins, hormones, growth factors, cytokines, serum albumin, haemoglobin, collagen, etc.

Thus the target gene or nucleotide sequence preferably encodes a target protein which is : an insect resistance protein; a disease resistance protein; a herbicide resistance protein; a mammalian protein.

Constructs & organisms

Preferably the target construct is a vector, and preferably it comprises border sequences which permit the transfer and integration of the expression cassette and MARs into the organism genome.

Preferably the construct is a plant binary vector. Preferably the binary transformation vector is based on pPZP (Hajdukiewicz, *et al.* 1994). Other example constructs include pBin19 (see Frisch, D. A., L. W. Harris-Haller, et al. (1995). "Complete Sequence of the binary vector Bin 19." Plant Molecular Biology 27: 405-409).

Preferably the construct used is substantially similar to pFAJ3163 shown in Figure 1 i.e. comprises the depicted features of that vector (or equivalents as described herein) in the recited order, and the

gene of interest in place of the the β-glucuronidase reporter gene (*uidA*). In embodiments in which endogenes are being activated by a promoter or enhancer element, the coding region of the construct may be absent.

In one aspect the invention may further comprise the step of regenerating a plant from a transformed plant cell.

Specific procedures and vectors previously used with wide success upon plants are described by Guerineau and Mullineaux (1993) (Plant transformation and expression vectors. In: Plant Molecular Biology Labfax (Croy RRD ed) Oxford, BIOS Scientific Publishers, pp 121-148). Suitable vectors may include plant viral-derived vectors (see e.g. EP-A-194809). If desired, selectable genetic markers may be included in the construct, such as those that confer selectable phenotypes such as resistance to antibiotics or herbicides (e.g. kanamycin, hygromycin, phosphinotricin, chlorsulfuron, methotrexate, gentamycin, spectinomycin, imidazolinones and glyphosate).

Nucleic acid can be introduced into plant cells using any suitable technology, such as a disarmed Ti-plasmid vector carried by Agrobacterium exploiting its natural gene transfer ability (EP-A-270355, EP-A-0116718, NAR 12(22) 8711 - 87215 1984; the floral dip method of Clough and Bent, 1998), particle or microprojectile bombardment (US 5100792, EP-A-444882, EP-A-434616) microinjection (WO 92/09696, WO 94/00583, EP 331083, EP 175966, Green *et al.* (1987) *Plant Tissue and Cell Culture*, Academic Press), electroporation (EP 290395, WO 8706614 Gelvin Debeyser) other forms of direct DNA uptake (DE 4005152, WO 9012096, US 4684611), liposome mediated DNA uptake (e.g. Freeman *et al. Plant Cell Physiol.* 29: 1353 (1984)), or the vortexing method (e.g. Kindle, *PNAS U.S.A.* 87: 1228 (1990d) Physical methods for the transformation of plant cells are reviewed in Oard,

1991, *Biotech. Adv.* 9: 1-11. Ti-plasmids, particularly binary vectors, are discussed in more detail below.

Agrobacterium transformation is widely used by those skilled in the art to transform dicotyledonous species. However there has also been considerable success in the routine production of stable, fertile transgenic plants in almost all economically relevant monocot plants (see e.g. Hiei *et al.* (1994) *The Plant Journal* 6, 271-282)). Microprojectile bombardment, electroporation and direct DNA uptake are preferred where Agrobacterium alone is inefficient or ineffective. Alternatively, a combination of different techniques may be employed to enhance the efficiency of the transformation process, eg bombardment with Agrobacterium coated microparticles (EP-A-486234) or microprojectile bombardment to induce wounding followed by co-cultivation with Agrobacterium (EP-A-486233).

The particular choice of a transformation technology will be determined by its efficiency to transform certain plant species as well as the experience and preference of the person practising the invention with a particular methodology of choice.

It will be apparent to the skilled person that the particular choice of a transformation system to introduce nucleic acid into plant cells is not essential to or a limitation of the invention, nor is the choice of technique for plant regeneration. In experiments performed by the inventors, the enhanced expression effect is seen in a variety of integration patterns of the T-DNA.

Thus various aspects of the present invention provide a method of transforming a plant cell involving introduction of a construct of the invention into a plant tissue (e.g. a plant cell) and causing or allowing recombination between the vector and the plant cell genome to introduce a nucleic acid according to the present invention into

the genome. This may be done so as to effect transient expression. Alternatively, following transformation of plant tissue, a plant may be regenerated, e.g. from single cells, callus tissue or leaf discs, as is standard in the art. Almost any plant can be entirely regenerated from cells, tissues and organs of the plant. Available techniques are reviewd in Vasil et al., *Cell Culture and Somatic Cell Genetics of Plants, Vol I, II and III, Laboratory Procedures and Their Applications*, Academic Press, 1984, and Weissbach and Weissbach, *Methods for Plant Molecular Biology*, Academic Press, 1989.

The generation of fertile transgenic plants has been achieved in the cereals rice, maize, wheat, oat, and barley (reviewed in Shimamoto, K. (1994) *Current Opinion in Biotechnology* 5, 158-162.; Vasil, *et al.* (1992) *Bio/Technology* 10, 667-674; Vain et al., 1995, *Biotechnology Advances* 13 (4): 653-671; Vasil, 1996, *Nature Biotechnology* 14 page 702).

Regenerated plants or parts thereof may be used to provide clones, seed, selfed or hybrid progeny and descendants (e.g. F1 and F2 descendants), cuttings (e.g. edible parts) etc.

The invention further provides a transgenic organism (for example obtained or obtainable by a method described herein) in which an heterologous target nucleotide sequence is expressed at an enhanced level,

wherein the organism is deficient in one or more genes required to support PTGS,

which organism includes in its genome (a) an expression cassette including the target nucleotide sequence operably linked to a promoter, and (b) one or more heterologous Matrix Attachment Regions (MARs) associated therewith.

The invention further comprises a method for generating a target protein, which method comprises the steps of performing a method (or using an organism) as described above, and optionally harvesting, at least, a tissue in which the target protein has been expressed and isolating the target protein from the tissue.

Definitions

"Matrix attachment region" (MARs) are non coding DNA sequences that are thought to mediate the binding of chromatin to the proteinaceous nuclear matrix, thereby creating chromatin domains as topologically isolated units of gene regulation.

The term "heterologous" is used broadly below to indicate that the gene/sequence of nucleotides in question have been introduced into the cells in question (e.g. of a plant or an ancestor thereof) using genetic engineering, i.e. by human intervention. A heterologous gene may replace an endogenous equivalent gene, i.e. one which normally performs the same or a similar function, or the inserted sequence may be additional to the endogenous gene or other sequence. Nucleic acid heterologous to a cell may be non-naturally occurring in cells of that type, variety or species. Thus the heterologous nucleic acid may comprise a coding sequence of, or derived from, a particular type of plant cell or species or variety of plant, placed within the context of a plant cell of a different type or species or variety of plant. A further possibility is for a nucleic acid sequence to be placed within a cell in which it or a homologue is found naturally, but wherein the nucleic acid sequence is linked and/or adjacent to nucleic acid which does not occur naturally within the cell, or cells of that type or species or variety of plant, such as operably linked to one or more regulatory sequences, such as a promoter sequence, for control of expression.

"Gene" unless context demands otherwise refers to any nucleic acid encoding genetic information for translation into a peptide, polypeptide or protein.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage, viral or *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform a prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication). The constructs used will be wholly or partially synthetic. In particular they are recombinant in that nucleic acid sequences which are not found together in nature (do not run contiguously) have been ligated or otherwise combined artificially. Unless specified otherwise a vector according to the present invention need not include a promoter or other regulatory sequence, particularly if the vector is to be used to introduce the nucleic acid into cells for recombination into the genome.

"Binary Vector": as is well known to those skilled in the art, a binary vector system includes (a) border sequences which permit the transfer of a desired nucleotide sequence into a plant cell genome; (b) desired nucleotide sequence itself, which will generally comprise an expression cassette of (i) a plant active promoter, operably linked to (ii) the target sequence and\or enhancer as appropriate. The desired nucleotide sequence is situated between the border sequences and is capable of being inserted into a plant genome under appropriate conditions. The binary vector system will generally require other sequence (derived from *A. tumefaciens*) to effect the integration. Generally this may be achieved by use of so called "agro-infiltration" which uses Agrobacterium-mediated transient transformation. Briefly, this technique is based on the property of *Agrobacterium tumefaciens* to transfer a portion of its DNA ("T-DNA")

into a host cell where it may become integrated into nuclear DNA. The T-DNA is defined by left and right border sequences which are around 21-23 nucleotides in length. The infiltration may be achieved e.g. by syringe (in leaves) or vacuum (whole plants). In the present invention the border sequences will generally be included around the desired nucleotide sequence (the T-DNA) with the one or more vectors being introduced into the plant material by agro-infiltration.

"Expression cassette" refers to a situation in which a nucleic acid is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial or plant cell.

A "promoter" is a sequence of nucleotides from which transcription may be initiated of DNA operably linked downstream (i.e. in the 3' direction on the sense strand of double-stranded DNA).

"Operably linked" means joined as part of the same nucleic acid molecule, suitably positioned and oriented for transcription to be initiated from the promoter.

It will be appreciated that where a nucleotide sequence (e.g. a specific MAR, gene, polypeptide, promoter etc.) is referred to or exemplified herein, the invention should not be taken to be limited to use of the recited sequence, but also embraces use of a variants of any of these sequences. A variant sequence will be identical to all or part of the sequence discussed and share the requisite activity, which activity can be confirmed using the methods disclosed or otherwise referred to herein or known to those skilled in the art. Generally speaking, wherever the term is used herein, variants may be (i) naturally occurring homologous variants of the relevant sequence; (ii) artificially generated variants (derivatives) which can be

prepared by the skilled person in the light of the present disclosure, for instance by site directed or random mutagenesis, or by direct synthesis. Preferably any variant sequence shares at least about 75%, or 80% identity, most preferably at least about 90%, 95%, 96%, 97%, 98% or 99% identity with that specifically refererred to. Similarity or homology in the case of variants is preferably established via sequence comparisons made using FASTA and FASTP (see Pearson & Lipman, 1988. Methods in Enzymology 183: 63-98). Parameters are preferably set, using the default matrix, as follows: Gapopen (penalty for the first residue in a gap): -12 for proteins / -16 for DNA; Gapext (penalty for additional residues in a gap): -2 for proteins / -4 for DNA; KTUP word length: 2 for proteins / 6 for DNA. Homology may also be assessed by use of a probing methodology (Sambrook et al., 1989). One common formula for calculating the stringency conditions required to achieve hybridization between nucleic acid molecules of a specified sequence homology is: T_m = 81.5°C + 16.6Log [Na+] + 0.41 (% G+C) - 0.63 (% formamide) - 600/#bp in duplex. As an illustration of the above formula, using [Na+] = [0.368] and 50-% formamide, with GC content of 42% and an average probe size of 200 bases, the T_m is 57°C. The T_m of a DNA duplex decreases by 1 - 1.5°C with every 1% decrease in homology. Thus, targets with greater than about 75% sequence identity would be observed using a hybridization temperature of 42°C.

The invention will now be further described with reference to the following non-limiting Figures and Examples. Other embodiments of the invention will occur to those skilled in the art in the light of these.

The disclosure of all references cited herein, inasmuch as it may be used by those skilled in the art to carry out the invention, is hereby specifically incorporated herein by cross-reference.

FIGURES

Figure 1

Schematic representation of the T-DNA region of plant transformation vectors pFAJ3160 and pFAJ3163. Not to scale. *UidA:* β-glucuronidase coding region; *pat:* phosphinothricin acetyltransferase coding region; p*NOS*: nopaline synthase promoter; p*35S*: cauliflower mosaic virus 35S promoter; t*OCS*: octopine synthase terminator; t*NOS*: nopaline synthase terminator; Chi1MAR: chicken lysozyme MAR; RB and LB: right and left T-DNA border, respectively.

Figure 2

GUS activity is expressed in units GUS (nmoles 4-methylumbelliferone per min per mg total soluble protein) in first generation transgenic *A. thaliana* wild-type, *sgs*2 and *sgs*3 background transformed with pFAJ3160 and pFAJ3163.

Figure 3

SDS-PAGE analysis of total protein extracts (2µg/lane) from *sgs*2 mutants transformed with pFAJ3163 (lanes 1 and 2); total protein extracts (2µg/lane) from non-transgenic plants (lane 3); 500ng bovine serum albumin (lane 4); partially purified β-glucuronidase (lane 5). The position of GUS is indicated by the arrow to the right. The position of molecular weight reference proteins is indicated by arrows to the left.

SEQUENCES

Where a DNA sequence is specified, unless context requires otherwise, use of the RNA equivalent, with U substituted for T where it occurs, is encompassed.

Sequence Annex 1: Chicken lysozyme MAR
Sequence Annex 2: pFAJ3160
Sequence Annex 3: pFAJ3163

EXAMPLES

Materials and methods

Briefly, a set of transformation vectors was constructed without and with MARs flanking the genes of interest. To quantify transgene expression the β-glucuronidase reporter gene (*uidA*) driven by the 35S promoter of Cauliflower Mosaic Virus (p35S) was used. For each plant transformation vector *A. thaliana* populations consisting of at least 30 primary transformants were obtained. The activity of the β-glucuronidase (GUS) enzyme in leaf extracts was measured and statistically evaluated.

Plant transformation vectors

All plant transformation vectors were constructed using the modular vector system as fully described in Goderis & De Bolle *et al.* (2002). pFAJ3160 and pFAJ3163 were assembled as previously described in De Bolle & Butaye *et al.* (2003) (see Sequence Annex).

Mutants

sgs2 and *sgs3* mutants as described in Elmayan *et al.* (1998) and Mourrain *et al.* (2000). Seeds of the mutants were provided by Hervé Vaucheret, INRA Versailles.

Plant Transformation

All plant transformation vectors were introduced in *Agrobacterium tumefaciens* GV3101 (pMP90) by electroporation. The *A. tumefaciens* strains with the binary vectors were used to transform *A. thaliana* wild-type and mutant plants using the floral dip transformation method as described by Clough & Bent (1998). Transgenic plants were selected based on resistance against phosphinotricin and further grown as described by De Bolle & Butaye *et al.* (2003).

Enzyme Assays

β-Glucuronidase (GUS) activity was measured fluorometrically using 4-methylumbelliferyl glucuronide as a substrate and 4-methylubmelliferon as a standard according to Jefferson (1987). Total protein was determined by the method of Bradford (1976) using bovine serum albumin as a standard.

SDS-PAGE

Total leaf extracts and GUS standard (Sigma-Aldrich) were separated on a 12.5% SDS-PAGE and visualized by staining with Coomassie brilliant blue R250.

Results

The A element that flanks the chicken lysozyme gene (Phi-Van *et al.*, 1990; chilMAR) has been shown to reduce transgene expression variability in tobacco (Mlynárová *et al.*, 1994). To test the effect

of chilMAR on transgene expression in *A. thaliana* plant transformation vectors without and with chilMARs flanking the T-DNA region were constructed, pFAJ3160 and pFAJ3163 respectively (Figure1).

ChilMAR in Col0

Transformation of wild-type *A. thaliana* plants with pFAJ3160 yielded an average GUS activity of 320 units (Table 1). The population of primary transformants consisted of about 80% low GUS expressing primary transformants (< 50 units GUS) and about 20% high GUS expressing primary transformants (>100 units GUS), a bimodal distribution typical for p*35S*-driven expression (Elmayan & Vaucheret, 1996; De Bolle & Butaye *et al.*, 2003; Figure 2A). To test the influence of chilMARs on transgene expression, wild-type plants were transformed with pFAJ3163. This resulted in a pattern of GUS activity similar to the one obtained with pFAJ3160 (Table 1; Figure 2B). It was concluded that chilMARs have no significant influence on the level of transgene expression or on the variability of transgene expression in populations of first generation wild-type *A. thaliana* transformants (De Bolle & Butaye *et al.*, 2003).

Table 1. GUS activity in first generation transgenic *Arabidopsis thaliana* wild-type, *sgs2* and *sgs3* background transformed with pFAJ3160 and pFAJ3163.

	GUS activity[a]			
	pFAJ3160 (- MAR)		pFAJ3163 (+ MAR)	
Background	No[b]	Mean ± S.E.[c]	No[b]	Mean ± S.E.[c]
Col0	36	320 ± 135	36	186 ± 81
sgs2	36	2280 ± 399	34	11 237 ± 1839
sgs3	33	830 ± 177	30	9994 ± 2006

[a] GUS activity is expressed in units GUS (nmoles 4-methylumbelliferone per min per mg total soluble protein). [b] Number of primary transformants analyzed. [c] S.E., Standard error.

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ChilMAR in *sgs2*

In a further attempt to elevate and level off transgene expression, *A. thaliana sgs2* mutants (Elmayan, *et al.*, 1998) were used as the recipient for transformation instead of wild-type plants. *SGS2* encodes an RNA dependent RNA polymerase, which is presumed to play a key role in RNA silencing of transgenes (Mourrain, *et al.* 2000). Using this mutant background for transformation with pFAJ3160, average GUS activity in primary transformants increased almost 8-fold compared to wild-type plants (Table 1). The increase in average GUS activity at the population level was not due to an increase in activity of the high-expressing individuals but rather to a reduction of the incidence of individuals with low expression. About 80% of the transformants in the wild-type background had a GUS activity below 50 units GUS, whereas all *sgs2* transformants had a GUS activity above 180 units GUS (Figure 2C). Upon transformation of *sgs2* mutants with pFAJ3163, chilMARs caused a 5-fold increase in average GUS activity compared to pFAJ3160 in *sgs2*. Compared to pFAJ3160 in wild-type plants, the chilMARs caused a 40-fold boost of mean GUS activity in *sgs2* mutants (Table 1; Figure 2D).

Some of the *sgs2* transformants containing chilMAR-flanked transgenes reached extremely high GUS activity levels, up to 41 000 units GUS. Coomassie blue staining of an SDS-PAGE gel revealed a clear band in the total leaf extracts of extremely high GUS expressing *sgs2* mutants (Figure 3, lanes 1 & 2), which is not visible in the total leaf extracts of non-transgenic control plants (Figure 3, lane 3) and which is situated at the same position in the gel as the GUS standard (Figure 3, lane 5). By densitometric comparison of the intensities of this band to known amounts of bovine serum albumin (BSA; Figure 3, lane 4) we estimate that GUS accumulated to roughly 10% of the total soluble protein in the transgenic *sgs2* plants.

ChilMAR in *sgs3*

SGS3 plays a yet unknown key role in the RNA silencing mechanism and shows no similarity with any known or putative protein (Mourrain, *et al.*, 2000). Using *sgs3* mutants for transformation with pFAJ3160, the average GUS activity was increased 2,5 fold in comparison the wild-type background (Table 1, Figure 2E). Transformation of *sgs3* plants with pFAJ3163 yielded a 30-fold increase of the average GUS activity in comparison to wild-type plants transformed with pFAJ3160.

References

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Sequence Annex 1: Chicken lysozyme MAR

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